SEQUENCE LISTING

<110> Loughney, Kate

<120> Phosphodiesterase 10

<130> 27866/35308

<140> 09/256,000
<141> 1999-02-23

<150> 60/075,508
<151> 1998-02-23

<160> 26

<170> PatentIn Ver. 2.0

<210> 1
<211> 1548
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (26)..(1423)

<400> 1
cccaaggcca tctacctgga catcg atg gac gca ttc aga agc act ccg tac   52
                             Met Asp Ala Phe Arg Ser Thr Pro Tyr
                             1   5

aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta   100
Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
 10   15   20   25

atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc   148
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
                30   35   40

aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta   196
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
            45   50   55

gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa   244
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
        60   65   70

tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc   292
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
    75   80   85

agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag   340
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
 90   95   100   105

aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc   388
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu

1

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tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg    436
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp
        125                      130                      135

ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac    484
Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His
        140                      145                      150

gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg    532
Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg
        155                      160                      165

agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac    580
Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His
170                      175                      180                      185

aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc    628
Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val
                190                      195                      200

tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc    676
Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile
                205                      210                      215

cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac    724
Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn
                220                      225                      230

aac acg tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat    772
Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn
        235                      240                      245

gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc    820
Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile
250                      255                      260                      265

ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg    868
Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly
                270                      275                      280

ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac    916
Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp
                285                      290                      295

atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag    964
Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu
        300                      305                      310

aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att    1012
Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile
        315                      320                      325

ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc    1060
Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val
330                      335                      340                      345
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2

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gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc    1108
Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser
            350                 355                 360

gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga    1156
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg
            365                 370                 375

gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc    1204
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val
            380                 385                 390

ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag    1252
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu
        395                 400                 405

gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag    1300
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
410                 415                 420                 425

ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac    1348
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
                430                 435                 440

agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat    1396
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp
            445                 450                 455

gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc gggggcgtg           1443
Val Lys Asn Ser Glu Gly Asp Cys Ala
            460                 465

gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc 1503

ctgggcacct ggcaccacaa gaccatgttt tctaagaacc atttt              1548


<210> 2
<211> 466
<212> PRT
<213> Homo sapiens

<400> 2
Met Asp Ala Phe Arg Ser Thr Pro Tyr Lys Val Arg Pro Val Ala Ile
  1               5                  10                  15

Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln
            20                  25                  30

Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala
            35                  40                  45

Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu
        50                  55                  60

Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
65                  70                  75                  80
```

3

Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
                85   90   95

Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp
            100   105   110

Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala
        115   120   125

Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met
    130   135   140

Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp
145   150   155   160

Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
            165   170   175

Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
            180   185   190

Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu
            195   200   205

Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys
    210   215   220

His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
225   230   235   240

Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn
            245   250   255

His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
            260   265   270

Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
            275   280   285

Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile
    290   295   300

Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu
305   310   315   320

Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
            325   330   335

Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys
            340   345   350

Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
            355   360   365

Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
    370   375   380

Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr

4

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           385                    390                    395                    400
Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
                405             410                 415

Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
            420             425                 430

Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr
        435             440                 445

Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp
    450                 455                 460

Cys Ala
465


<210> 3
<211> 225
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 130, 186, and 205 are
      either A, T, G, or C.

<400> 3
agcgaccgtg agaagtcaga aggccttcct gtggaaccgt tcatggaccg agacaaagtg 60

accaaggcca cagcccagat tgggttcatc aagtttgccc tgatcccaat gtttgaaaca 120

gtgaccaagn tcttccccat ggttgaggag atcatgctgc agccactttg ggaatcccga 180

gatcgntacg aggagctgaa gcggntagat gacgccatga aagag            225


<210> 4
<211> 158
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 12, 36, 61, and 109 are
      either A, T, G, or C.

<400> 4
gtaccagatc antgcccgca cagagctggc ggtccgntac aatgacatct caccgttgga 60

gnaaccacca ctgcgccgtg gccttccaga tcctcgccga gcctgagtgn aacatcttct 120

ccaacatccc acctgatggg ttcaagcaga tccgacag                158


<210> 5
<211> 98
<212> DNA
<213> Homo sapiens
```

<220>
<223> Nucleotides at positions 14, 22, and 50 are either
      A, T, C, or G.

<400> 5
gagaacacca ctgngccgtg gncttccaga tcctcgccga gcctgagtgn aacatcttct 60

ccaacatccc acctgatggg ttcaagcaga tccgacag   98

<210> 6
<211> 418
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 267, 352, 400, and 411
      are either A, T, G, or C.

<400> 6
nggttaactg gcgcatcttg tctttctctg agaacagcga tctggttatg gggcatttct 60

gtctctaatg tcactgtctg ctgcattccc tgcagagcga ccgtgagaag tcagaaggcc 120

ttcccgtggc cccgttcatg gaccgagaca aagtgaccaa ggccacagcc caggattggg 180

tttcatcaag tttgtcctga tcccaatgtt tgaaacagtg accaagctct tccccatggg 240

ttgagggaga ttcatgctgg cagccanttt ggggaatccc gaggattcgc tacgagggag 300

cttgaagcgg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360

acagttttga agttttgggg gggccaccga ggaagttccn ggaggaggag naggcaga 418

<210> 7
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 82, 92, 130, 347, 390,
      and 396 are either A, T, G, or C.

<400> 7
nagaaaaaag tgaacaaaat ggttcttaga aaacatggtc ttgtggtgcc aggtgcccag 60

ggagctcttc cctgcacaag gntcccgcgc antcggccag cccgtccaga actgcagcca 120

cgccccccgn tttcctcagg cacagtctcc ttcactgttt ttcacatctc tgcttctctc 180

tctggacttc tcggtggccc cagacgtcaa gctgtcagtc ttcttctgta actctttcat 240

gggcgtcatc tatccgcttc agctcctcgt aggcgatctc ggggattccc aaagtgggct 300

gcagcatgat cttcctcaac catggggggg aggagcttgg ggcactngtt ttcaaaaatt 360

gggggatcag gggacaaact ttgattggan cccatnttgg ggcttttggg cctttggggc 420

<210> 8
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 63, 98, 107, 188, 203,
      206, 238, 252, 297, 370, 389, and 427 are either
      A, T, G, or C.

<400> 8
tttttttttt tttttttttgt atcagtgaac aaaatggttc ttagaaaaca tggtcttgtg 60

gtnccaggtg cccagggagc tcttccctgc acaaggancc cgcgcantcg gccagcccgt 120

ccagaactgc agccacgccc cccgttttcc tcaggcacag tctccttcac tgttttcac 180

atctctgntt ctctctctgg ganttntcgg tgggccccag aacgtcaagc tgtcagtntt 240

cttctgtaac tntttcatgg gcgtcatcta tccgtttcag cttcctcgta ggcgatnttg 300

gggattccca aagtgggctg gcagcatgga tcttcctcaa accatggggg gaaggagttt 360

gggtcaattn ttttcaaaac attgggggnt cagggacaaa attttgatgg aaacccaatt 420

tggggggntgt gggccttg   438

<210> 9
<211> 262
<212> DNA
<213> Mus musculus

<400> 9
gagaattttg actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaa 60

tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120

ttactggaag aatattttat gcagagtgac cgtgagaagt ccgaagcctt cctgtggccc 180

cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagtttg 240

tcctgatccc aatgtttgaa ac   262

<210> 10
<211> 250
<212> DNA
<213> Mus musculus

<400> 10
gagaattttg actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaa 60

tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120

ttactggaag aatattttat gcagagtgac cgtgagaagt ccgaagcctt cctgtggccc 180

attcatggac cgagacaaag tgaccaaagc aacagccaaa ttgggttcat caagtttgtc 240

tgtccaatgt   250

<210> 11
<211> 459
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 155, 393, and 442 are
      either A, T, G, or C.

<400> 11
attaatcttg gccactgaca tggcaagaca tgcagaaatt atggattctt tcaaagagaa 60

aatggagaat tttgactaca gcaacgagga gcacatgacc ctggtgagtg gcttattctg 120

cctgggtggg cagccaggcg gttgggctgg cgaanaggtt catccatcca gctcacactg 180

gaagccaaga agctgaaatt attagtcttc ttggaacaag gtgtctataa atctggtttt 240

caaggtcatg actcttacta ggaaagtccg ggcagggcct ccctcctgat gggtcctcct 300

tcatggtcag aggcagcatt ctcccattcc tccatctctt ttgggatttt gaaggagata 360

aagtggggtg aaggccgtgc attctcgctc tgnttttcca gagaattaaa accagttttc 420

ccttgaaggc acagccccag cntggcattt tgaaagttg   459

<210> 12
<211> 599
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (99)..(443)

<400> 12
tggccctcga ggccaagaat tcggcacgag tggttaactg gcgcatcttg tctttctctg 60

agaacagcga tctggttatg gggcatttct gtctctaa tgt cac tgt ctg ctg cat 116
                                          Cys His Cys Leu Leu His
                                           1   5

tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg 164
Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
           10   15   20

ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc 212
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
     25   30   35

8

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atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc    260
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
        40                  45                  50

ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat    308
Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
 55                  60                  65                  70

cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag    356
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
                75                  80                  85

aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag    404
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu
                90                  95                  100

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc     453
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
            105                 110                 115

ggggggcgtg gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg   513

aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca   573

ctgatacaaa aaaaaaaaaa aaaaaa                                        599


<210> 13
<211> 115
<212> PRT
<213> Homo sapiens

<400> 13
Cys His Cys Leu Leu His Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu
 1               5                  10                  15

Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala
                20                  25                  30

Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu
            35                  40                  45

Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro
 50                  55                  60

Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp
 65                  70                  75                  80

Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala
                85                  90                  95

Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly
            100                 105                 110

Asp Cys Ala
        115
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9

<210> 14
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
agtcgaattc accgtgagaa gtcagaag   28

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
gtcaaagctt acatggtctt gtggtgcc   28

<210> 16
<211> 1303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (107)..(1066)

<400> 16
agtgactcta ctttgtgaaa atgtgaaact tcgtgtaggt actcagtaaa tcagtaaatt 60

cttactaacg ttagccccca gcctagctat ggagggtgca tgctga gcc ctg gag   115
                                                     Ala Leu Glu
                                                      1

cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163
His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
      5   10   15

gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
 20   25   30   35

aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg 259
Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met
              40   45   50

tac agc atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa acg 307
Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr
              55   60   65

gat atc ctg atc cta atg aca gcg gcc atc tgc cac gat ctg gac cat 355
Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His

ccc ggc tac aac aac acg tac cag atc aat gcc cgc aca gag ctg gcg   403
Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala
         85   90   95

gtc cgc tac aat gac atc tca ccg ctg gag aac cac cac tgc gcc gtg   451
Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val
100   105   110   115

gcc ttc cag atc ctc gcc gag cct gag tgc aac atc ttc tcc aac atc   499
Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile
                120   125   130

cca cct gat ggg ttc aag cag atc cga cag gga atg atc aca tta atc   547
Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile
                135   140   145

ttg gcc act gac atg gca aga cat gca gaa att atg gat tct ttc aaa   595
Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys
                150   155   160

gag aaa atg gag aat ttt gac tac agc aac gag gag cac atg acc ctg   643
Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu
        165   170   175

ctg aag atg att ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt   691
Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg
180   185   190   195

cca atg gaa gtc gca gag cct tgg gtg gac tgt tta tta gag gaa tat   739
Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr
                200   205   210

ttt atg cag agc gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg   787
Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
                215   220   225

ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc   835
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
                230   235   240

atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc   883
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
        245   250   255

ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat   931
Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
260   265   270   275

cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag   979
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
                280   285   290

aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag   1027
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu
                295   300   305

11

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc   1076
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
      310   315   320

ggggggcgtg gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg   1136

aagagctgcc ctgggcacct ggcaccacaa gaccatgttt ctaagaacc attttgttca   1196

ctgatacaaa aaaaaaaaag gaattcatga tgctgtacag aatttttattt ttaaactgtc   1256

ttttaaataa tatattctta tacggaaaaa aaaaaaaaaa aaaaaaa   1303

<210> 17
<211> 320
<212> PRT
<213> Homo sapiens

<400> 17
Ala Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser
  1   5   10   15

Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn
        20   25   .   30

Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala
        35   40   45

Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe
     50   55   60

Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp
  65   70   75   80

Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr
          85   90   95

Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His
          100   105   110

Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe
         115   120   125

Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile
         130   135   140

Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp
145   150   155   160

Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His
         165   170   175

Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn
         180   185   190

Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu
         195   200   205

12

```
Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro
    210             215         '           220

Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln
225             230             235             240

Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr
                245             250             255

Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu
            260             265             270

Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys
        275             280             285

Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys
    290             295             300

Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
305             310         .       315             320
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<400> 18
ctccccgcc tcccgcggcg gctggcgtcg ggaaagtaca gtaaaaagtc cgagtgcagc   60

cgccgggcgc agg atg gga tcc ggc tcc tcc agc tac cgg ccc aag gcc       109
            Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala
             1               5                   10

atc tac ctg gac atc gat gga cgc att cag aag gta atc ttc agc aag     157
Ile Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys
         15                  20                  25

tac tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc     205
Tyr Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly
     30                  35                  40

ctg cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg     253
Leu Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met
 45                  50                  55                  60

gtc tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac     301
Val Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr
                 65                  70                  75

aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta     349
Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
             80                  85                  90
```

13

```
atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc    397
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
        95              100             105

aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta    445
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
    110             115             120

gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa    493
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
125             130             135             140

tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc    541
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
                145             150             155

agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag    589
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
            160             165             170

aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc    637
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
        175             180             185

tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg    685
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp
        190             195             200

ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac    733
Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His
205             210             215             220

gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg    781
Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg
                225             230             235

agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac    829
Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His
                240             245             250

aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc    877
Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val
            255             260             265

tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc    925
Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile
    270             275             280

cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac    973
Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn
285             290             295             300

aac acg tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat   1021
Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn
            305             310             315

gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc   1069
Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile
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14

```
ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg    1117
Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly
        335                     340                 345

ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac    1165
Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp
    350                     355                 360

atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag    1213
Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu
365                 370                 375                 380

aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att    1261
Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile
                    385                 390                 395

ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc    1309
Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val
            400                 405                 410

gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc    1357
Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser
        415                 420                 425

gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga    1405
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg
    430                 435                 440

gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc    1453
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val
445                 450                 455                 460

ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag    1501
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu
                465                 470                 475

gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag    1549
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
            480                 485                 490

ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac    1597
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
        495                 500                 505

agc ttg acg tct ggg gcc acc gag aag tcc aga gag aga agc aga gat    1645
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp
    510                 515                 520

gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc gggggcgtg          1692
Val Lys Asn Ser Glu Gly Asp Cys Ala
525                 530

gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc  1752

ctgggcacct ggcaccacaa gaccatgttt ctaagaacc attttgttca ctgataaaaa   1812
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aaaaaaaaaa ggaattcatg atgctgtaca gaattttatt tttaaactgt cttttaaata 1872

atatattctt atacg   1887

<210> 19
<211> 533
<212> PRT
<213> Homo sapiens

<400> 19
Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp
 1   5   10   15

Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
            20   25   30

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
        35   40   45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
    50   55   60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
65   70   75   80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
                85   90   95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
            100   105   110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
        115   120   125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
    130   135   140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
145   150   155   160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
                165   170   175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
            180   185   190

Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
        195   200   205

Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
    210   215   220

Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
225   230   235   240

Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
                245   250   255

16

Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
            260   265   270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
        275   280   285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
    290   295   300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
305   310   315   320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
            325   330   335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
            340   345   350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
            355   360   365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
    370   375   380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
385   390   395   400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
            405   410   415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys
            420   425   430

Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr
        435   440   445

Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met
    450   455   460

Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu
465   470   475   480

Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
            485   490   495

Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser
            500   505   510

Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser
        515   520   525

Glu Gly Asp Cys Ala
    530

<210> 20
<211> 1967
<212> DNA

17

<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(1741)

<400> 20
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c tac ctg gac atc gat gga cgc att cag aag gta atc ttc agc aag tac   49
  Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr
   1               5                   10                  15

tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc ctg    97
Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
             20                  25                  30

cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg gtc   145
Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
         35                  40                  45

tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac aaa   193
Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
     50                  55                  60

gtg aga cct gtg gcc atc aag caa ctc tcc gct gat gtc gag gac aag   241
Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
 65                  70                  75                  80

aga acc aca agc cgt ggc cag tct gct gag aga cca ctg agg gac aga   289
Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
                 85                  90                  95

cgg gtt gtg ggc ctg gag cag ccc cgg agg gaa gga gca ttt gaa agt   337
Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
                100                 105                 110

gga cag gta gag ccc agg ccc aga gag ccc cag ggc tgc tac cag gaa   385
Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
            115                 120                 125

ggc cag cgc atc cct cca gag aga gaa gaa tta atc cag agc gtg ctg   433
Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
        130                 135                 140

gcg cag gtt gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg   481
Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
145                 150                 155                 160

aaa gct gaa gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa   529
Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
                165                 170                 175

ttg gaa gga cta aaa gtg gtg gag att gag aaa tgc aag agt gac att   577
Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
                180                 185                 190

aag aag atg agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc   625
Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
            195                 200                 205
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18

```
ccc tgt aag tac agt ttt ttg gat aac cac aag aag ttg act cct cga    673
Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg
    210                 215                 220

cgc gat gtt ccc act tac ccc aag tac ctg ctc tct cca gag acc atc    721
Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile
225                 230                 235                 240

gag gcc ctg cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat    769
Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn
                245                 250                 255

gag atg ctg agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc    817
Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val
                260                 265                 270

agg gac ttc agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc    865
Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys
                275                 280                 285

gtc cac gac aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc    913
Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
    290                 295                 300

ttc tgc gtg gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc    961
Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
305                 310                 315                 320

cag gag aag ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc    1009
Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
                325                 330                 335

atc tgc cac gat ctg gac cat ccc ggc tac aac aac acg tac cag atc    1057
Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile
                340                 345                 350

aat gcc cgc aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg    1105
Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
                355                 360                 365

gag aac cac cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag    1153
Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
    370                 375                 380

tgc aac atc ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga    1201
Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
385                 390                 395                 400

cag gga atg atc aca tta atc ttg gcc act gac atg gca aga cat gca    1249
Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
                405                 410                 415

gaa att atg gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc    1297
Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
                420                 425                 430

aac gag gag cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt    1345
Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
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19

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gat atc tct aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg   1393
Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
    450             455             460

gac tgt tta tta gag gaa tat ttt atg cag agc gac cgt gag aag tca   1441
Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
465             470             475             480

gaa ggc ctt cct gtg gca ccg ttc atg gac cga gac aaa gtg acc aag   1489
Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
            485             490             495

gcc aca gcc cag att ggg ttc atc aag ttc gtc ctg atc cca atg ttt   1537
Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
        500             505             510

gaa aca gtg acc aag ctc ttc ccc atg gtt gag gag atc atg ctg cag   1585
Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
        515             520             525

cca ctt tgg gaa tcc cga gat cgc tac gag gag ctg aag cgg ata gat   1633
Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
    530             535             540

gac gcc atg aaa gag tta cag aag aag act gac agc ttg acg tct ggg   1681
Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
545             550             555             560

gcc acc gag aag tcc aga gag aga agc aga gat gtg aaa aac agt gaa   1729
Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
            565             570             575

gga gac tgt gcc tgaggaaagc gggggcgtg gctgcagttc tggacgggct   1781
Gly Asp Cys Ala
            580

ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc ctgggcacct ggcaccacaa   1841

gaccatgttt tctaagaacc attttgttca ctgatacaaa aaaaaaaaa ggaattcatg   1901

atgctgtaca gaattttatt tttaaactgt cttttaaata atatattctt atacggaaaa   1961

aaaaaa                                                              1967
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<210> 21
<211> 580
<212> PRT
<213> Homo sapiens

<400> 21
Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr
 1               5               10              15

Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
            20              25              30
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Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
                35   40   45

Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
       50   55   60

Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65   70   75   80

Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
                85   90   95

Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
                100   105   110

Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
       115   120   125

Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
       130   135   140

Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
145   150   155   160

Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
                165   170   175

Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
                180   185   190

Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
                195   200   205

Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg
       210   215   220

Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile
225   230   235   240

Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn
                245   250   255

Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val
                260   265   270

Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys
                275   280   285

Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
       290   295   300

Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
305   310   315   320

Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
                325   330   335

Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile

21

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              340                    345                    350

Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
        355                 360                 365

Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
    370                 375                 380

Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
385                 390                 395                 400

Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
                405                 410                 415

Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
                420                 425                 430

Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
        435                 440                 445

Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
        450                 455                 460

Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
465                 470                 475                 480

Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
                485                 490                 495

Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
                500                 505                 510

Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
                515                 520                 525

Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
        530                 535                 540

Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
545                 550                 555                 560

Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
                565                 570                 575

Gly Asp Cys Ala
            580


<210> 22
<211> 1457
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (164)..(1453)

<400> 22
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22

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ggctcccggg cgtcccgggc ccggtggcgg cgcggctgtg gttggctgag cgccgcgggc  60

cgcccccgc ccgcccctc ccctgctccc ctcccccgcc tcccgcggcg gctggcgtcg  120

ggaaagtaca gtaaaaagtc cgagtgcagc cgccgggcgc agg atg gga tcc ggc  175
                                             Met Gly Ser Gly
                                              1

tcc tcc agc tac cgg ccc aag gcc atc tac ctg gac atc gat gga cgc  223
Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg
 5                  10                  15                  20

att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg  271
Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met
                 25                  30                  35

gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc  319
Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser
             40                  45                  50

ctg ctg acc acc gac gac gcc atg gtc tcc atc gac ccc acc atg ccc  367
Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro
         55                  60                  65

gcg aat tca gaa cgc act ccg tac aaa gtg aga cct gtg gcc atc aag  415
Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys
     70                  75                  80

caa ctc tcc gag aga gaa gaa tta atc cag agc gtg ctg gcg cag gtt  463
Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val
 85                  90                  95                 100

gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg aaa gct gaa  511
Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu
                105                 110                 115

gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa ttg gaa gga  559
Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly
             120                 125                 130

cta aaa gtg gtg gag att gag aaa tgc aag agt gac att aag aag atg  607
Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met
         135                 140                 145

agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc ccc tgt aag  655
Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys
     150                 155                 160

tac agt ttt ttg gat aac cac aag aag ttg act cct cga cgc gat gtt  703
Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val
165                 170                 175                 180

ccc act tac ccc aag tac ctg ctc tct cca gag acc atc gag gcc ctg  751
Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu
                185                 190                 195

cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat gag atg ctg  799
Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu
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23

agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc agg gac ttc   847
Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe
        215   220   225

agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac   895
Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp
    230   235   240

aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg   943
Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val
245   250   255   260

gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc cag gag aag   991
Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys
                265   270   275

ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc atc tgc cac   1039
Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His
                280   285   290

gat ctg gac cat ccc ggc tac aac aac acg tac cag atc aat gcc cgc   1087
Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg
            295   300   305

aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg gag aac cac   1135
Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His
    310   315   320

cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag tgc aac atc   1183
His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile
325   330   335   340

ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga cag gga atg   1231
Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met
                345   350   355

atc aca tta atc ttg gcc act gac atg gca aga cat gca gaa att atg   1279
Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met
                360   365   370

gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc aac gag gag   1327
Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu
            375   380   385

cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt gat atc tct   1375
His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser
    390   395   400

aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg gac tgt tta   1423
Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu
405   410   415   420

tta gag gaa tat ttt atg cag agc gac cgt gaga   1457
Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg
            425   430

24

<210> 23
<211> 430
<212> PRT
<213> Homo sapiens

<400> 23
Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp
1   5   10   15

Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
                20   25   30

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
            35   40   45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
    50   55   60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
65   70   75   80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
                85   90   95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
            100   105   110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
        115   120   125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
    130   135   140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
145   150   155   160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
                165   170   175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
            180   185   190

Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
        195   200   205

Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
    210   215   220

Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
225   230   235   240

Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
            245   250   255

Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
            260   265   270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala

25

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
    290   295   300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
305   310   315   320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
            325   330   335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
            340   345   350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
            355   360   365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
    370   375   380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
385   390   395   400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
            405   410   415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg
            420   425   430

<210> 24
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<220>
<223> Description of Artificial Sequence: FLAG epitope

<400> 24
Asp Thr Lys Asp Asp Asp Asp Lys
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<210> 25
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<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 25
tagaccatgg actacaagga cgacgatgac aagatggacg cattcagaag cact   54

<210> 26
<211> 18
<212> DNA

26

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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cgaggagtca acttcttg   18